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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 C.F.R § 1.53(b))

Attorney Docket No.	6752.US.O1
First Inventor or Application Identifier	Stephen W. Fesik
Title	MUTANT BCL-2 PROTEINS AND USES THEREOF
Express Mail Label No.	EL507389345US

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO: Assistant Commissioner for Patents, Box Patent Application, Washington, DC 20231

1. [X] * Fee Transmittal Form (e.g., PTO/SB/17) (Submit an original and a duplicate for fee processing)
2. [X] Specification [Total Pages 23] (preferred arrangement set forth below)
   - Descriptive title of the Invention
   - Cross References to Related Applications
   - Statement Regarding Fed sponsored R & D
   - Reference to Microfiche Appendix
   - Background of the Invention
   - Brief Summary of the Invention
   - Brief Description of the Drawings (if filed)
   - Detailed Description
   - Claim(s)
   - Abstract of the Disclosure
3. [X] Drawing(s) (35 U.S.C. 113) [Total Sheets 3]
4. Oath or Declaration [Total Pages 3]
   a. [X] Newly executed (original or copy)
   b. [ ] Copy from a prior application (37 C.F.R. § 1.63(d)) (for continuation/divisional with Box 16 completed)
      i. [ ] DELETION OF INVENTOR(S) Signed statement attached deleting inventor(s) named in the prior application, see 37 C.F.R. §§ 1.63(d)(2) and 1.33(b).

***NOTE FOR ITEMS 1 & 13 IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C.F.R. § 1.27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C.F.R. § 1.28).**

5. [ ] Microfiche Computer Program (Appendix)
6. Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary)
   a. [X] Computer Readable Copy
   b. [X] Paper Copy (identical to computer copy)
   c. [X] Statement verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

7. [ ] Assignment Papers (cover sheet & document(s))
8. [ ] 37 C.F.R.§3.73(b) Statement (when there is an assignee) [ ] Power of Attorney
9. [ ] English Translation Document (if applicable)
10. [ ] Information Disclosure Statement (IDS)/PTO-1449 [ ] Copies of IDS Citations
11. [ ] Preliminary Amendment
12. [X] Return Receipt Postcard (MPEP 503) (Should be specifically itemized)
13. [ ] * Small Entity Statement(s) (PTO/SB/09-12) [ ] Statement filed in prior application Status still proper and desired
14. [ ] Certified Copy of Priority Document(s) (if foreign priority is claimed)
15. [ ] Other: ....

16. **If a CONTINUING APPLICATION,** check appropriate box, and supply the requisite information below and in a preliminary amendment

[ ] Continuation [ ] Divisional [ ] Continuation-in-part (CIP) of prior application No: ______/______

Prior application information: Examiner ______ Group / Art Unit: ______

For CONTINUATION or DIVISIONAL APPS only: The entire disclosure of the prior application, from which an oath or declaration is supplied under Box 4b, is considered a part of the disclosure of the accompanying continuation or divisional application and is hereby incorporated by reference. The incorporation can only be relied upon when a portion has been inadvertently omitted from the submitted application parts.

17. CORRESPONDENCE ADDRESS

[ ] Customer Number or Bar Code Label (Insert Customer No or Attach bar code label here) or [ ] Correspondence address below

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Signature	Dianne Casuto	Date	November 20, 2000

Practitioner's Docket No. 6752.US.O1 *PATENT*

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Stephen W. Fesik, *et al.*

Serial No.: Group No.:
Filed: November 20, 2000 Examiner:

For: **MUTANT BCL-2 PROTEINS AND USES THEREOF**

Box Patent Application
Assistant Commissioner for Patents
Washington, D.C. 20231

EXPRESS MAIL CERTIFICATE

"Express Mail" label number EL507389345US
Date of Deposit: November 20, 2000

I hereby state that the following *attached* papers or fees

Utility Patent Application Transmittal – 1 pg.
Fee Transmittal, 1 pg. (in duplicate)
Specification (19 pages); Claims (3 pages); Abstract (1 page); **Total: 23pages**
Drawings – Figures 1-3 (3 pages)
Paper copy of Sequence Listing – 11 pgs.
Computer Readable Form Copy of Sequence Listing – 1 disc
Statement to Support filings and Submission in Accordance with 37 CFR 1.821 through 1.825 – 1 pg.
Executed Declaration and Power of Attorney - 3 pages
Two Return-Receipt Postcards

are being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10, on the date indicated above and is addressed to the Box Patent Application, Assistant Commissioner for Patents, Washington, D.C. 20231.

Wanda E. Smith

Wanda E. Smith

Signature of person mailing paper or fee

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FEE TRANSMITTAL

Patent fees are subject to annual revision on October 1. These are the fees effective October 1, 1997
Small Entity payments must be supported by a small entity statement, otherwise large entity fees must be paid See Forms PTO/SB/09-12 See 37 C.F R §§1.27 and 1.28.

TOTAL AMOUNT OF PAYMENT ($) 710.00

Complete if Known	
Application Number	
Filing Date	November 20, 2000
First Named Inventor	Stephen W. Fesik
Examiner Name	(not yet assigned)
Group / Art Unit	(not yet assigned)
Attorney Docket No.	6752.US.O1

09/716395 11/20/00

METHOD OF PAYMENT (check one)

1. [X] The Commissioner is hereby authorized to charge indicated fees and credit any over payments to:

Deposit Account Number: 01-0025
Deposit Account Name: Abbott Laboratories

[X] Charge Any Additional Fee Required Under 37 C F.R §§ 1.16 and 1 17
[ ] Charge the Issue Fee Set in 37 C.F R §1 18 at the Mailing of the Notice of Allowance

2. [ ] **Payment Enclosed:** [ ] Check [ ] Money Order [ ] Other

FEE CALCULATION

1. BASIC FILING FEE

Large Entity Fee Code	Large Entity Fee ($)	Small Entity Fee Code	Small Entity Fee ($)	Fee Description	Fee Paid
101	790	201	395	Utility filing fee	710.00
106	330	206	165	Design filing fee	
107	540	207	270	Plant filing fee	
108	790	208	395	Reissue filing fee	
114	150	214	75	Provisional filing fee	

SUBTOTAL (1) ($) 710.00

2. EXTRA CLAIM FEES

			Extra Claims		Fee from below		Fee Paid
Total Claims	18	-20** =	0	X	18.00	=	00.00
Independent Claims	3	- 3** =	0	X	80.00	=	00.00
Multiple Dependent						=	

***or number previously paid, if greater, For Reissues, see below*

Large Entity Fee Code	Large Entity Fee ($)	Small Entity Fee Code	Small Entity Fee ($)	Fee Description
103	22	203	11	Claims in excess of 20
102	82	202	41	Independent claims in excess of 3
104	270	204	135	Multiple dependent claim, if not paid
109	82	209	41	** Reissue independent claims over original patent
110	22	210	11	** Reissue claims in excess of 20 and over original patent

SUBTOTAL (2) ($) 00.00

FEE CALCULATION (continued)

3. ADDITIONAL FEES

Large Entity Fee Code	Large Entity Fee ($)	Small Entity Fee Code	Small Entity Fee ($)	Fee Description	Fee Paid
105	130	205	65	Surcharge - late filing fee or oath	
127	50	227	25	Surcharge - late provisional filing fee or cover sheet.	
139	130	139	130	Non-English specification	
147	2,520	147	2,520	For filing a request for reexamination	
112	920*	112	920*	Requesting publication of SIR prior to Examiner action	
113	1,840*	113	1,840*	Requesting publication of SIR after Examiner action	
115	110	215	55	Extension for reply within first month	
116	400	216	200	Extension for reply within second month	
117	950	217	475	Extension for reply within third month	
118	1,510	218	755	Extension for reply within fourth month	
128	2,060	228	1,030	Extension for reply within fifth month	
119	310	219	155	Notice of Appeal	
120	310	220	155	Filing a brief in support of an appeal	
121	270	221	135	Request for oral hearing	
138	1,510	138	1,510	Petition to institute a public use proceeding	
140	110	240	55	Petition to revive - unavoidable	
141	1,320	241	660	Petition to revive - unintentional	
142	1,320	242	660	Utility issue fee (or reissue)	
143	450	243	225	Design issue fee	
144	670	244	335	Plant issue fee	
122	130	122	130	Petitions to the Commissioner	
123	50	123	50	Petitions related to provisional applications	
126	240	126	240	Submission of Information Disclosure Stmt	
581	40	581	40	Recording each patent assignment per property (times number of properties)	
146	790	246	395	Filing a submission after final rejection (37 CFR 1.129(a))	
149	790	249	395	For each additional invention to be examined (37 CFR 1.129(b))	

Other fee (specify) ______________________

Other fee (specify) ______________________

*Reduced by Basic Filing Fee Paid

SUBTOTAL (3) ($) 0

SUBMITTED BY				Complete (if applicable)	
Typed or Printed Name	Dianne Casuto			Reg. Number	40,943
Signature	Dianne Casuto	Date	November 20, 2000	Deposit Account User ID	

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MUTANT BCL-2 PROTEINS AND USES THEREOF

Technical Field of The Invention

The present invention relates to mutant Bcl-2 proteins derived from wild-type human Bcl-2. The proteins of the present invention can be used in biological assays to identify substances which block the ability of Bcl-2 to inhibit programmed cell death.

Background of the Invention

Apoptosis or programmed cell death (hereinafter "PCD") is a highly conserved and essential feature of development and homeostasis in higher organisms. Kelekar, et al., *Molecular and Cellular Biology*, 17(12):7040-7046 (1997). Apoptosis is a mechanism by which the body replaces older cells with new healthy cells, or by which a cell destroys itself to prevent the transmission of genetic errors to its progeny. In some cancers, for example, it is generally accepted that an alteration in cell growth and/or cell death is due to the accumulation of several mutations in "key" genes which regulate these processes. The normal system is unable to eliminate cells containing these mutated genes and uncontrolled cell growth results. Thus, the aberrant nature of cell growth or apoptosis observed in cancer and other diseases is the consequence of malfunctioning of the regulatory pathways which control the equilibrium between cell growth and cell death.

One group of molecules that is involved in promoting or suppressing apoptotic responses is the Bcl-2 family of proteins. The Bcl-2 family contains proteins which either promote or inhibit cell death. Some of the inhibitors, frequently referred to as anti-apoptotic proteins, include: Bcl-2, Bcl-x_L, Mcl-1, adenovirus E1B 19K, Epstein-Barr virus BHRF1, and *Caenorhabditis elegans* Ced-9. Promoters of cell death, frequently referred to as pro-apoptotic proteins, include, for example: Bax, Bak, Bad, Bik, Bid and Bcl-x_S An important feature of the Bcl-2 family is that its members can interact (i.e. dimerize) with themselves or other members of the family. (Kelekar, *supra*. Also see Ottilie, S., et al., *J. of Biol. Chem.*, 272(49):30866-30872 (1997)). It is believed that these protein-protein interactions are critically important in determining a cell's response to a death signal (Kelekar, *supra*, also see Yang et al., *Cell*, 80:285-291 (1995)).

The three-dimensional structure of the Bcl-2 family member, Bcl-x_L has been

elucidated (Muchmore et al., *Nature,* 381:335-341 (1996)). The structure of Bcl-x_L contains two central hydrophobic helices surrounded by amphipathic helices. A hydrophobic binding pocket, is created by the spatial proximity of three particular domains, known as BH1, BH2, and BH3, and provides a binding site for the death-promoting proteins. Sattler M., et al., *Science,* 275:983-986 (1997). It is also known that the death-promoting proteins interact with this binding site through their BH3 domains. *Id.*

It is known in the art that over-expression of the anti-apoptotic proteins, such as Bcl-2 and Bcl-$x_{L,}$ which are often present in cancerous and other diseased cells, results in the blocking of apoptotic signals and allows said cells to proliferate. For example, high levels of Bcl-2 gene expression are found in a wide variety of human cancers. Furthermore, it is believed that by blocking Bcl-2 and Bcl-$x_{L,}$ apoptosis can be induced in diseased cells, and can provide an effective therapy for cancer and other diseases caused by the impairment of the apoptotic process. Thereupon, there is a need in the art for an assay, which can be used to identify compounds which trigger or induce apoptosis by inhibiting the interactions between the Bcl-2 family of proteins.

It is also known in the art that naturally occurring or wild-type Bcl-2 behaves poorly and aggregates when placed in solution. Such aggregation makes it difficult for researchers to use Bcl-2 in structural studies such as X-ray crystallography or NMR which can aid in the design of drugs which block the ability of Bcl-2 to inhibit programmed cell death. Additionally, the aggregation of Bcl-2 in solution also makes it difficult to use naturally occurring or wild-type Bcl-2 protein in assays to identify substances which block the ability of Bcl-2 to inhibit programmed cell death. Therefore, there is a need in the art to develop an altered or mutated form of Bcl-2 that does not aggregate in solution and which can be used in structural studies. However, thus far, efforts to develop such an altered or mutated protein have been unsuccessful. For example, Anderson et al. in *Protein Expression and Purification*, 15:162-170 (1999), describe the cloning and expression of a recombinant human Bcl-2 referred to as "*rh*Bcl-2". In this mutant form of Bcl-2, the putative flexible loop of Bcl-2 is truncated and replaced with a flexible linker which consists of four (4) alanine residues. In addition, the hydrophobic carboxy terminus of Bcl-2 is replaced with six (6) histidine residues. Specifically, the Anderson et al. Bcl-2 deletion mutant can be summarized as follows: Bcl-2 $_{(6-32)}$ – AAAA-Bcl-2 $_{(56-206)}$ – HHHHHH. While Anderson et al. were able to

successfully express their mutant in *E. coli* and purify it, they noted that the solubility limit for their expressed protein was lower than ideal for X-ray or NMR-based structural studies under the examined conditions. Thereupon, a need currently exists in the art for an altered or mutant form of Bcl-2 which can be used in X-ray or NMR-based structural studies. There is also a need for screening assays to identify compounds that are capable of binding to Bcl-2. Such screening assays can be achieved with a water soluble Bcl-2 mutant.

Summary of the Invention

The present invention relates to a mutant protein derived from a wild-type human Bcl-2 protein. More specifically, in the mutant proteins of the present invention, a sequence of amino acid residues comprising a flexible loop from the wild-type human Bcl-2 protein is replaced with a different sequence (i.e. a replacement amino acid sequence) comprising at least two acidic amino acids. The acidic amino acids may be glutamic acid or aspartic acid or a combination of both. Preferably, the replacement amino acid sequence comprises a sequence of at least a portion of a flexible loop from human Bcl-x_L protein. More preferably, the replacement amino acid sequence comprises the sequence of SEQ ID NO:1. A particularly preferred mutant protein has the amino acid sequence of SEQ ID NO:2.

In one embodiment of the invention, the replacement amino acid sequence of the mutant protein comprises a sequence of at least 4 to about 50 amino acid residues. More preferably, the replacement amino acid sequence comprises a sequence of at least 16 to about 25 amino acid residues.

The mutant proteins of the invention have an isoelectric point lower than that of wild-type Bcl-2. Preferably, the isoelectric point is from 4.5 to about 6.0 and more preferably, from 5.0 to about 5.5. A particularly preferred isoelectric point is 5.0.

The present invention also relates to an assay for identifying substances which bind to a Bcl-2 protein, the assay comprising the steps of (a) providing a candidate substance to be tested; (b) providing a labeled peptide which is capable of binding tightly to a mutant protein of the invention; (c) forming a complex of the labeled peptide with the mutant protein; (d) forming a reaction mixture by contacting the candidate substance with the labeled peptide/mutant protein complex; (e) incubating the reaction mixture under conditions sufficient to allow the candidate substance to react and displace the labeled peptide; and (f)

determining the amount of labeled peptide that has been displaced from binding to said mutant protein. Preferably, the peptide is labeled with a radioisotope, fluorescent moiety, enzyme, specific binding molecule or particle. More preferably, the peptide is labeled with a fluorescein compound. Most preferably, the peptide is labeled with fluorescein isothiocyanate or 5-carboxy-fluorescein.

Brief Description of the Figures

Figure 1 shows the wild-type amino acid sequences for the Bcl-2 isoforms 1, 2, and 3 (hereinafter Bcl-2/iso1 (SEQ ID NO:3), Bcl-2/iso2 (SEQ ID NO:4), and Bcl-2/iso3 (SEQ ID NO:5, respectively) and the wild-type sequence of human Bcl-x_L protein. The differences between Bcl-2/iso1, Bcl-2/iso2, and Bcl-2/iso3 are highlighted in bold. The putative unstructured loop (amino acid residues 35-91) is underlined.

Figure 2 shows a Ribbons representation of wild-type human Bcl-x_L. The unstructured loop is shown as the uncoiled ribbon projecting to the left in the Figure.

Figure 3 shows a Ribbons representation of the NMR-derived structure of (A) Bcl-2/iso1 and (B) Bcl-2/iso2.

Detailed Description of the Invention

1. The Present Invention

The present invention relates to mutant Bcl-2 proteins which do not aggregate in solution and can be used in assays to identify substances which bind to a Bcl-2 protein.

II. Sequence Listing

The present application also contains a sequence listing. For the nucleotide sequences, the base pairs are represented by the following base codes:

Symbol	Meaning
A	A; adenine
C	C; cytosine
G	G; guanine
T	T; thymine
U	U; uracil
M	A or C
R	A or G
W	A or T/U

Symbol	Meaning
S	C or G

Symbol	Meaning
Y	C or T/U
K	G or T/U
V	A or C or G; not T/U
H	A or C or T/U; not G
D	A or G or T/U; not C
B	C or G or T/U; not A
N	(A or C or G or T/U)

The amino acids shown in the application are in the L-form and are represented by the following amino acid-three letter abbreviations:

Abbreviation	Amino acid name
Ala	L-Alanine
Arg	L-Arginine
Asn	L-Asparagine
Asp	L-Aspartic Acid
Asx	L-Aspartic Acid or Asparagine
Cys	L-Cysteine
Glu	L-Glutamic Acid
Gln	L-Glutamine
Glx	L-Glutamine or Glutamic Acid
Gly	L-Glycine
His	L-Histidine
Ile	L-Isoleucine
Leu	L-Leucine
Lys	L-Lysine
Met	L-Methionine
Phe	L-Phenylalanine
Pro	L-Proline
Ser	L-Serine
Thr	L-Threonine
Trp	L-Tryptophan
Tyr	L-Tyrosine
Val	L-Valine
Xaa	L-Unknown or other

III. Proteins of the Present Invention

The present invention relates to mutant Bcl-2 proteins derived from the naturally occurring or wild-type human Bcl-2 protein. More specifically, the mutant proteins of the present invention are chimeric proteins that contain amino acid residues derived from wild-type human Bcl-2 protein but which exhibit a lower isoelectric point than the wild-type

protein. Accordingly, unlike naturally occurring or wild-type human Bcl-2 protein, the mutant Bcl-2 proteins of the present invention do not aggregate in solution. In a preferred embodiment, the mutant proteins of the present invention comprise amino acid residues derived from wild-type human Bcl-x_L protein as well as from the naturally occurring or wild-type human Bcl-2 protein. Because the mutant Bcl-2 proteins of the present invention do not aggregate when placed in solution, these proteins can be used in X-ray crystallography and NMR structural studies as well as in assays to identify candidate compounds which block the ability of Bcl-2 to inhibit programmed cell death.

As used herein, the term "isoelectric point" (or pI) refers to the pH at which the protein carries no net charge. The isoelectric points of Bcl-2/iso1, Bcl-2/iso2, and Bcl-2/iso3 are about 7.0, 7.2 and 7.2, respectively. The mutant proteins of the present invention have an isoelectric point lower than that of wild-type Bcl-2 and preferably, in the range of 4.5 to about 6.0. More preferably, the isoelectric point of a mutant protein of the invention is from 4.5 to about 5.5. A more preferred isoelectric point is from about 5.0 to about 5.5. A most preferred isoelectric point is 5.0. Means for determining the isoelectric point of a protein are well known to those of ordinary skill in the art.

As used herein, the term "naturally occurring" or "wild-type" human Bcl-2 protein refers to any of three proteins which are isoforms of human Bcl-2. These isoforms are shown as SEQ ID NOS:3, 4, and 5. The protein shown in SEQ ID NO:3 is referred to as "isoform 1" (Bcl-2/iso1) and is described in Tsujimoto, Y. *et al.*, *Science*, 226:1097-1099 (1984) and Tsujimoto, Y. *et al.*, *PNAS,* **83:**5214-5218 (1986). The protein shown in SEQ ID NO:4 is referred to as "isoform 2" (Bcl-2/iso2) and is described in Cleary, M. and Sklar. K., *PNAS*, **82:**7439-7443 (1985) and Cleary, M. *et al.*, *Cell,* **47:**19-28 (1986). The protein shown in SEQ ID NO:5 is referred to as "isoform 3" (Bcl-2/iso3) and is described in Bakshi, A. *et al.*, *Cell*, **41:**899-906 (1985) and Seto, M. *et al.*, *EMBO J.* **7:**123-131(1988). As can be seen in Fig. 1, Bcl-2/iso3 differs from Bcl-2/iso1 and Bcl-2/iso2 at residue position 48 (F in place of I). Bcl-2/iso1 differs from the other two isoforms at residue positions 96 and 110 (A and G in place of T and R, respectively).

As used herein, the term "naturally occurring" or "wild-type" human Bcl-x_L protein refers to the protein shown in SEQ ID NO:**6** and described in *Cell*, **74:**597-608 (1993).

As used herein, the term "about", when used to modify an isoelectric point, means

±5%. When used to modify a length of amino acid sequence, "about" means ±2 amino acids.

Naturally occurring or wild-type human Bcl-x_L protein contains an unstructured flexible loop (meaning, that it shows no regular secondary structure such as an α-helix or β-sheet) that is not required for maintaining the integrity of the protein in solution (Muchmore et al., *Nature,* 381:335-341 (1996)). This loop is found at amino acid residues 35-91 (see Figure 1 and SEQ ID NOS:**6**). It is known in the art that the Bcl-x_L protein retains it function as an anti-apoptotic protein even when this loop is removed from the protein. Based on the sequence homology between Bcl-x_L and Bcl-2, residues 35-91 of Bcl-2 also are presumed to be unstructured and unnecessary for maintaining the integrity of the protein. These unstructured loops are points of post-translational modification such as phosphorylation.

The mutant proteins of the present invention are derived from human Bcl-2 protein. Specifically, the mutant human Bcl-2 proteins of the present invention have the amino acid residues which form its unstructured, flexible loop replaced with at least 4 to about 50 amino acid residues of which at least two are acidic amino acids, i.e. glutamic acid (Glu) or aspartic acid (Asp). The acidic amino acids may be located at any position within the replacement sequence. Furthermore, the replacement sequence may comprise only one type of acidic amino acid (i.e. either two or more Glus or two or more Asps) or a combination of both. As intended by this description, there is no limit on the type or total number of acidic amino acids comprising the replacement sequence (as long as it comprises at least two acidic amino acids).

In a preferred embodiment, the unstructured, flexible loop of the human Bcl-2 protein is replaced with a sequence of at least 4 to about 50 amino acid residues corresponding to a contiguous sequence of amino acid residues from the unstructured loop of Bcl-x_L wherein at least two of the residues are acidic amino acids. More preferably, the amino acid residues of the unstructured, flexible loop of Bcl-2 are replaced with at least 16 to about 25 amino acid residues (of which at least two are acidic amino acids) from the corresponding, unstructured, flexible loop from human Bcl-x_L protein. Even more preferably, the entire sequence of the unstructured, flexible loop of Bcl-2, from amino acid residues 35-91, is replaced with the sequence DVEENRTEAPEGTESE (SEQ ID NO:1) which encode a portion of the flexible loop of the naturally occurring or wild-type human Bcl-x_L protein:.

The mutant Bcl-2 proteins of the present invention can contain from about 150 to

about 180 amino acid residues.

An example of a preferred mutant Bcl-2 protein of the present invention includes, but is not limited to:

MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDDVEENRTEAPEGTESEVVHLA LRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGRFATVVEELFRDGVNWGRIVAFFEF GGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVELYGPSMR (SEQ ID NO:2).

As discussed previously, the mutant Bcl-2 proteins of the present invention do not aggregate in solution unlike the naturally occurring or wild-type Bcl-2 protein. While not wishing to be bound by any theory, the inventors of the present invention believe that that the substitution of a portion of the unstructured, flexible loop from the human Bcl-x_L protein for the entire unstructured, flexible loop from Bcl-2, makes the mutant Bcl-2 proteins of the present invention more acidic and thus reduces the isoelectric point of the mutant Bcl-2 proteins compared to the naturally occurring or wild-type Bcl-2 protein. More specifically, the inventors found that when amino acid residues 49-91 were removed from the unstructured flexible loop of Bcl-x_L, this shortened protein behaved well in solution and did not aggregate. The isoelectric point of this shortened Bcl-x_L protein was determined to be about 4.9. The inventors then removed the same amino acid residues (49-91) from the unstructured, flexible loop of Bcl-2. Surprisingly, this shortened protein did not behave well in solution and exhibited aggregation. The isoelectric point of this shortened Bcl-2 protein was determined to be about 6.4. The inventors compared the shortened loops of the Bcl-x_L and Bcl-2 proteins and realized that the shortened loop from Bcl-x_L contained more acidic amino acid residues than the shortened loop from Bcl-2, thus giving the shortened Bcl-x_L protein a lower isoelectric point than the shortened Bcl-2 protein. The inventors believe that the difference in the isoelectric points explains the difference in the behavior of the two proteins.

The mutant proteins of the present invention have an isoelectric point below about 6.0, preferably below about 5.5. More specifically, the inventors found that when the entire sequence of the unstructured, flexible loop of Bcl-2, from amino acid residues 35-91 is replaced with the amino acid residues DVEENRTEAPEGTESE (SEQ ID NO:1) (which represent a portion of the flexible loop of the naturally occurring or wild-type human Bcl-x_L protein), the isoelectric point of this mutant Bcl-2 protein is about 5.0. The inventors believe

that this reduction in the isoelectric point in the mutant Bcl-2 protein of the present invention when compared to the wild-type Bcl-2 protein accounts for why the mutant Bcl-2 proteins do not aggregate in solution.

The mutant proteins of the present invention can be prepared using techniques known in the art, such as by recombinant DNA techniques. For example, a nucleotide sequence encoding a Bcl-2 mutant protein as described above, can be inserted into a suitable DNA vector, such as a plasmid. More specifically, the nucleotide sequence can be inserted into a suitable DNA vector using techniques known in the art, including, but not limited to, blunt-ending or staggered-ending termini for ligation, restriction enzyme digestion to provide appropriate termini, filling in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and ligation with appropriate ligases. Techniques for such manipulations are described in Sambrook, J., et al., *Molecular Cloning: A Laboratory Manual,* 2d Ed., Cold Spring Harbor Laboratory Press, Plainview, N.Y., (1989). Once prepared the nucleotide sequence is inserted into the DNA vector, the vector is used to transform a suitable host. The recombinant mutant protein is produced in the host by expression. The transformed host can be either a prokaryotic or eukaryotic cell.

Once the proteins of the present invention have been prepared, they may be substantially purified by a number of chromatographic procedures, including ion exchange, affinity, size exclusion or hydrophobic interaction (see Crighton, T., *Proteins, Structures and Molecular Principles*, WH Freeman and Co., New York, N.Y. (1983)). The composition of any synthetic proteins of the present invention can be confirmed by amino acid analysis or sequencing (using the Edman degradation procedure). The mutant proteins of the present invention can be used in screening assays. More specifically, the mutant proteins of the present invention can be used to identify small molecules that block the ability of Bcl-2 to inhibit programmed cell death.

IV. Screening Assays Using the Proteins of the Present Invention

The present invention also relates to a variety of screening assays to identify candidate compounds that are capable of binding to the mutant Bcl-2 proteins of the present invention and thus inhibit programmed cell death. The assay of present invention focuses on the ability or inability of candidate compounds to bind to the mutant Bcl-2 proteins of the present

invention and displace a labeled probe molecule such as a peptide.

The screening assays of the present invention can be used to screen large numbers of compounds to identify those compounds which are capable of binding to Bcl-2. Compounds which are identified as binding to Bcl-2 can be used clinically as anti-cancer agents. Specifically, these compounds can be used to promote apoptosis in cancer cells that over express Bcl-2 the treatment of certain cancers. Compounds which do not have activity in the screening assays can be eliminated from further consideration as candidate compounds.

The candidate compounds to be screened can encompass numerous chemical classes. However, the candidate compounds are typically organic molecules, preferably small organic compounds having a molecular weight of from about 150 to about 800 daltons. Such candidate compounds shall contain functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate compounds often contain cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate compounds can also be found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof.

Candidate compounds can be obtained from a wide variety of sources such as libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and oligopeptides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means, and may be used to produce combinatorial libraries. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, etc., to produce structural analogs.

In competitive binding assays, the candidate compound can compete with a labeled analyte for specific binding to sites on a binding agent bound to a solid surface. In such an assay, the labeled analyte can be a labeled peptide and the binding agent can be the mutant

Bcl-2 protein of the present invention bound to the solid phase. The concentration of labeled analyte bound to the binding agent is inversely proportional to the ability of the candidate compound to compete in the binding assay. The amount of inhibition of labeled analyte by the candidate compound depends on the binding assay conditions and on the concentrations of binding agent, labeled analyte, and candidate compound that are used. Under specified assay conditions, a candidate compound is said to be capable of binding to the mutant Bcl-2 protein of the present invention in a competitive binding assay, if the amount of binding of the labeled analyte to the binding agent is decreased by ten percent (10%) or more. In a direct binding assay, a candidate compound binds to the mutant Bcl-2 protein of the present invention when the signal measured is twice the background level or higher.

In a competitive binding assay, the candidate compound competes with the labeled analytes for binding to the mutant Bcl-2 protein of the present invention. As described herein, the binding agent can be bound to a solid surface to effect separation of bound labeled analyte from the unbound labeled analyte. Alternatively, the competitive binding may be conducted in a liquid phase, and any of a variety of techniques known in the art may be used to detect the release of the bound labeled analyte or to separate the bound labeled analyte from the unbound labeled analayte. Following separation, the amount of bound labeled analyte is determined. The amount of protein present in the sample is inversely proportional to the amount of bound labeled analyte.

Alternatively, a homogenous binding assay can be performed in which a separation step is not needed. In these types of assays, binding of the candidate compound to the mutant Bcl-2 protein results in displacement of a labeled analyte, and subsequent change in signal emitted by the analyte.

An example of a competitive binding assay for detecting candidate compounds capable of binding of the mutant Bcl-2 proteins of the present invention is described in Example 2 herein.

As discussed hereinbefore, the screening assays described herein employ one or more labeled molecules. The label used in the assay of the present invention can directly or indirectly provide a detectable signal. Various labels that can be used include radioisotopes, fluorescent compounds, chemiluminescent compounds, bioluminescent compounds, enzymes, specific binding molecules, particles, e.g., magnetic particles, and the like. Specific

binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin, etc. For the specific binding members, the complementary member is normally labeled with a molecule that provides for detection, in accordance with known procedures. Furthermore, the binding of these labels to the mutant proteins of the present invention is accomplished using standard techniques known in the art.

A variety of other reagents may also be included in the screening assay. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. that are used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Reagents that improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components are added in any order that provides for the requisite binding. Incubations are performed at any suitable temperature, typically between about 0 and about 40°C. Incubation periods are selected for optimum activity. Typically, incubations from about 0.05 and 10 hours will be sufficient.

By way of example, and not of limitation, examples of the present invention shall now be given.

EXAMPLE 1: Preparation of Mutant Bcl-2 Proteins

Construction of plasmids. Nucleic acid constructs were prepared for producing mutant Bcl-2 proteins which were subsequently evaluated for their suitability for NMR structural studies. All reagents used in the generation of these constructs were obtained from commercially available sources. Generally, nucleic acid fragments were prepared by standard PCR techniques and cloned into commercial vectors by means well known in the art. All sequences were confirmed by analysis on an ABI Prism 377 DNA sequencer (PE Applied Biosystems, Foster City, CA). The forward and reverse primers used to amplify the PCR fragments are shown in Table I below.

Table 1

Fragment Sequence	SEQ ID NO:
5'-CACTCACCATATGGCTCACGCTGGGAGAACGGGGTACGACAAC-3'	7
5'-GCGAGCTCTCGAGCTTCAGAGACAGCCAGGAGAAATCAAACAG-3'	8

5'-GCCCCAGAAGGGACTGAATCGGAGGTGGTCCACCTGGCCCTCCGCCAA-3'	9
5'-CTCAGTACGGTTCTCTTCCACATCATCTCCCGCATCCCACTCGTAGCC-3'	10
5'-CACTCACCATATGGCTCACGCTGGGAGAACGGGGTACGACAAC-3'	11
5'-GCGAAGCTCTCGAGCTATCAATCAAACAGAGGCCGCATGCTGGGGCCGTA-3'	12
5'-GAGGTGGTCCACCTGACCCTCCGCCAAGCCG-3'	13
5'-CGGCTTGGCGGAGGGTCAGGTGGACCACCTC -3'	14
5'-GCCGCTACCGCCGCGACTTCGCCGAG-3'	15
5'-CTCGGCGAAGTCGCGGCGGTAGCGGC-3'	16

A fragment encoding amino acids 1-218 of Bcl-2 first was prepared by reverse transcriptase polymerase chain reaction (RT-PCR), using an RT-PCR kit from BOEHRINGER-MANNHEIM Corp. (Indianapolis, IN). The fragment was generated using primer sequences SEQ ID NO:**7** and SEQ ID NO:**8** and Daudi mRNA (CLONTECH, Palo Alto, CA) as a template, under conditions suggested by the manufacturer. The fragment initially was cloned into NdeI and XhoI sites of the plasmid pET30b (Novagen, Madison, WI) for expression. The resulting plasmid was termed plasmid A.

A second plasmid (plasmid B) then was generated which contained fragments encoding amino acids 1-34 of SEQ ID NO:**3** (Bcl-2/iso1), amino acids 29-44 of SEQ ID NO:**6** (Bcl-x_L loop) and 92-218 of SEQ ID NO:**3** (Bcl-2/iso1). The fragments were generated with an ExpandLong PCR kit (BOEHRINGER-MANNHEIM Corp., Indianapolis, IN) using SEQ ID NOS:**9** and **10** as primers, plasmid A as template and the following cycle conditions: One cycle at 94°C, 4 min., one cycle at 94°C, 40 sec., 15 cycles at 55°C, 45 sec; 68°C, 6 min and 1 cycle at 72°C, 10 min. The primer sequences were designed in such a manner so as to (1) amplify in a "backward" direction in order to omit the intervening sequence of plasmid A (containing the nucleotides which encode for amino acids 35-91 of SEQ ID NO: **3**) and (2) contain nucleotides which encode for the Bcl-x_L loop (amino acids 29-44 of SEQ ID NO: **6**). Subsequent ligation of the amplified fragment resulted in plasmid B.

A third plasmid (plasmid C) was constructed which contained a fragment encoding amino acids 1-34 of SEQ ID NO:**3** (Bcl-2/iso1), amino acids 29-44 of SEQ ID NO:**6** (Bcl-x_L loop) and 92-207 of SEQ ID NO: **3** (Bcl-2/iso1). A fragment was generated from plasmid B (as template), using standard PCR reagents, Pfu DNA polymerase, and SEQ ID NOS:**11** and **12** as primers with the following cycle conditions: One cycle at 94°C, 4 mins., thirty cycles at

94°C, 30 sec.; 55°C, 45 sec; 72°C, 2 min., one cycle at 72°C, 10 min.. The resulting fragment was cloned into the NdeI and XhoI sites of pET28b (Novagen, Madison, WI), forming plasmid C.

For constructing the plasmid for Bcl-2/iso2 (plasmid D), plasmid C was used as a DNA template. Alanine 96 and glycine 110 were changed to threonine 96 and arginine 110 respectively, using two sets of primers: SEQ ID NOS:**13** and **14** (for the Ala96 to Thr96 mutation) and SEQ ID NOS:**15** and **16** (for the Gly110 to Arg 110 mutation). The mutated sequences were obtained using a Stratagene® Quick Change kit (Stratagene®, La Jolla, CA) in accordance with the manufacturer's directions.

<u>Expression and purification of Bcl-2 mutein</u>: The Bcl-2 muteins were expressed *in E. coli* BL21(DE3) cells grown in M9 medium containing $^{15}NH_4Cl$, $^{15}NH_4Cl$ plus [U-^{13}C]glucose, or $^{15}NH_4Cl$, [U-^{13}C]glucose, and 75% ^2H_2O. Cells were induced with 1mM isopropyl-D-thioglactopyranoside for 3 hours at 30°C during mid-log phase. Cells were resuspended in 20 mM Tris-Cl, pH 7.8, 1.5 M NaCl, 5mM 2-mercaptoethanol, and then lysed by French Press. The soluble fraction was loaded over Ni^{2+}-agarose column, washed with the same column buffer, then washed with 20 mM imidazole, 20 mM Tris-Cl, pH 7.8, 1.5 M NaCl, 5 mM 2-mercaptoethanol, and finally eluted with 500mM imidazole, 20 mM Tris-Cl pH 7.8, 5 mM 2-mercaptoethanol. The eluted Bcl-2 fraction was treated with biotinylated thrombin according to the suggested protocol of the manufacturer (Novagen, Madison, WI). Biotinylated thrombin (0.5 units) was used to cleave 1 mg of protein for 16 hours at room temperature. The cleavage reaction was stopped by adding Streptavidin Agarose (Novagen, Madison, WI), diluted three fold with 20 mM Tris-Cl, pH 7.5, and passed over another pre-equilibrated Ni^{2+} column. The non-his tagged flow through Bcl-2 fraction was collected. The purified Bcl-2 mutein was concentrated and stored at 4°C. N-terminal protein sequencing for the purified Bcl-2 mutein was carried out on 477A Protein Sequencer (PE Applied Biosystem, Forster City, Ca). The protein concentration was determined using a Coomassie protein assay kit from Pierce (Rockford, IL) and UV.

EXAMPLE 2: Competitive Binding Assays to Measure Peptide Affinities for Bcl-2/iso1

A competitive fluorescence polarization assay was used to measure the affinity of various peptides for Bcl-2/iso1 (see Table 2) or Bcl-2/iso2 (see Table 3). Competitive assays were performed using one of the following three fluorescein-labeled peptides as a probe:

(1) (5-FAM)-AAAAAQRYGRELRRMSDEFVDSFKK(SEQ ID NO:**17**), obtained from Synpep Corporation, Dublin, CA,

(2) (5-FAM)-AAAAAQRYGRELRRMSDEFVDSKK (SEQ ID NO:**18**), or

(3) (FITC)-AAQRYGRELRRMSDEFVR(SEQ ID NO:**19**). The dissociation constants of these fluoresceinated peptides from Bcl-2/iso1 are ~ 20 nM, ~ 50 nM, and ~ 100 nM, respectively.

All titrations were automated by means of an Abbott clinical diagnostics instrument (IMx, FPIA mode) modified with a special protocol for performing titrations. A complete two-fold dilution series, comprised of twenty separate 2 mL samples, was obtained by delivering appropriate individual aliquots to the first seven tubes, aliquots from an intermediate diluted stock for the next seven, and one more intermediate dilution for the final six. Dilution buffer for all stocks and samples was 120 mM sodium phosphate at pH 7.55 with 0.01% bovine gamma globulin and 0.1% sodium azide. The concentrations of the DMSO stock solutions of the peptide were 1-4 mM as determined by Trp absorbance (O.D. 280 nm), Tyr absorbance (O.D. 293), or amino acid analysis. The final DMSO concentration for all samples never exceeded 1%. Twenty 1.8 uL samples were prepared without fluoresceinated peptide and read as blanks. To each tube, 0.2 uL of a Bcl-2, fluoresceinated peptide mixture was added; the tubes were incubated for 5 min at 35° C, and then read for total intensity and polarization. Free and bound values for the fluoresceinated peptide were constant within a range ± 5 mP. Final Bcl-2 concentration was 340 nM. Comparisons with other, lower Bcl-2 concentrations, were made for the wild type Bcl-2 peptide. Additional controls using buffer lacking BGG showed that non-specific binding to BGG was negligible.

Steady state polarization data can be analyzed to extract the fractions of bound and free fluorescent ligand owing to the linear additivity of their anisotropy values, weighted by their respective fractional intensities (Lakowicz, JR. *Principles of Fluorescence Spectroscopy*. New York, NY: Plenum Press (1983)). Nonlinear least squares curve fitting of titration data to a model for simple equilibrium binding of the fluoresceinated peptide to Bcl-2 was accomplished by programming standard binding equations, solved in terms of bound,

free, and observed anisotropy values, into the model development program MINSQ (V. 4.03, Micromath Scientific Software). To determine affinities of nonfluorescent peptides, the analytical approach for equilibrium competition binding taken by Dandliker and coworkers was used, again employing MINSQ for fitting of titration curves (Dandliker, et al., *Methods in Enzymology* 74: 3 – 28 (1981)). Confirmation of the validity of these experimental and fitting procedures was obtained by comparing results after performing fluorescenated peptide binding, and competition binding titrations at different fixed Bcl-2 or fluorescenated peptide concentrations.

Table 2: Peptide Binding to Bcl-2/iso1

Sequence	SEQ. ID NO:	K_d (nM)
NLWAAQRYGRELRRMSDEFVDSFKK	**20**	14
ALWAAQRYGRELRRMSDEFVDSFKK	**21**	211
NAWAAQRYGRELRRMSDEFVDSFKK	**22**	75
NLAAAQRYGRELRRMSDEFVDSFKK	**23**	39
AAAAAQRYGRELRRMSDEFVDSFKK	**17**	74
NLWGAQRYGRELRRMSDEFVDSFKK	**24**	159
NLWAGQRYGRELRRMSDEFVDSFKK	**25**	105
NLWAAQRYGRELRRMSDEFVDAFKK	**26**	26
NLWAAQRYGRELRRMSDEFVDSAKK	**27**	397
NLWAAQRYGRELRRMSDEFVDSFAK	**28**	123
NLWAAQRYGRELRRMSDEFVDSFKA	**29**	22
GGGAAQRYGRELRRMSDEFVDSFKK	**30**	63
NLPAAQRYGRELRRMSDEFVDSFKK	**31**	54
NLWAAQRYARELRRMSDEFVAAFKK	**32**	186
NLWAAQRYGREARRMSDEFVDSFKK	**33**	7483
NLWAAQRYGRELRRMSAEFVDSFKK	**34**	762
QRYGRELRRMSDEFVDSFKK	**35**	711
NLWAAQRYGRELRRMSDEFVD	**36**	2326

Table 3: Peptide Binding to Bcl-2/iso2

Sequence	SEQ. ID NO:	K_d (nM)
NLWAAQRYGRELRRMSDEFVDSFKK	**20**	8
GQVGRQLAIIGDDINR	**37**	1600

As Tables 2 and 3 show, the mutant proteins of the invention can be used for identifying compounds which bind tightly to a Bcl-2 family member.

EXAMPLE 3: Structure Determination of Bcl-2/iso1 and Bcl-2/iso2 by NMR

<u>NMR Spectroscopy</u>: The structures of soluble Bcl-2/iso1 and Bcl-2/iso2 were determined by NMR spectroscopy (see Figure 3). All NMR experiments were acquired at 298 K on a Bruker DRX500, DRX600 or DRX800 NMR spectrometer. Backbone ^{1}H, ^{13}C, and ^{15}N resonance assignments were achieved with [^{15}N,^{13}C,(75%)^{2}H] Bcl-2 using a suite of deuterium-decoupled, triple-resonance experiments (HNCA, HN(CO)CA, HN(CA)CB, HN(COCA)CB, HNCO and HN(CA)CO) (Yamazaki, T., Lee, W., Arrowsmith, C. H., Muhandiram, D. R. & Kay, L. E. (1994) *J. Am. Chem. Soc.* **116,** 11655-11666). The side-chain ^{1}H and ^{13}C NMR signals were assigned from HCCH-TOCSY experiments (Clore, G. M. & Gronenborn, A. M. (1994) *Methods Enzymol* **239,** 349-63), and stereospecific assignments of the valine and leucine methyl groups were obtained from an analysis of the ^{13}C-^{13}C coupling patterns observed for biosynthetically directed, fractionally ^{13}C-labeled Bcl-2 (Neri, D., Szyperski, T., Otting, G., Senn, H. & Wüthrich, K. (1989) *Biochemistry* **28,** 7510-7516). NOE distance restraints were obtained from three-dimensional ^{15}N- and ^{13}C-edited NOESY spectra (Fesik, S. W. & Zuiderweg, E. R. P. (1988) *J. Magn. Reson.* **78,** 588-593, Marion, D., Driscoll, P. C., Kay, L. E., Wingfield, P. T., Bax, A., Gronenborn, A. M. & Clore, G. M. (1989) *Biochemistry* **29,** 6150-6156) acquired with a mixing time of 80 ms. Slowly exchanging amide protons were identified in an ^{15}N-HSQC spectrum recorded immediately after exchanging the protein into a buffer prepared with D_2O. Residual dipolar couplings (HN-N and C'-C$^{\alpha}$) were measured using undecoupled versions of the HNCO experiment on [^{15}N,^{13}C,(75%)^{2}H] Bcl-2 in the presence of 17 mg mL^{-1} Pf1 phage (Tjandra, N. (1999) *Structure* **7,** R205-R211, Hansen, M. R., Mueller, L. & Pardi, A. (1998)

Nature Struc. Biol. **5,** 1065-1074, Clore, G. M., Starich, M. R. & Gronenborn, A. M. (1998) *J. Am. Chem. Soc.* **120,** 1-571-10572).

Structure Calculations: Bcl-2 structures were calculated using a simulated annealing protocol (Brunger, A. T. (1992) *X-PLOR Version 3.1.* (Yale University Press, New Haven and London) with the program CNX (MSI, San Diego). A square-well potential (F_{NOE} = 50 kcal mol^{-1}) was employed to constrain NOE-derived distances. Based on the cross peak intensities, NOE-derived distance restraints were given upper bounds of 3.0, 4.0, 5.0, or 6.0 Å. Torsion angle restraints ϕ,ψ were generated from analysis of N, C', C^{α}, and H^{α} chemical shifts using the TALOS program (Cornilescu, G., Delaglio, F. & Bax, A. (1999) *J. Biomol. NMR* **13,** 289-302). A force constant of 200 kcal mol^{-1} rad^{-2} was applied to all torsional restraints. Explicit hydrogen bonds were included in α-helices only for residues observed to have slowly exchanging amide protons. The program PROCHECK was employed to analyze the geometric quality of the calculated structures in the ensemble (Laskowski, R. A., MacArthur, M. W., Moss, D. S. & Thornton, J. M. (1993) *J. Appl. Cryst.* **26,** 283-291).

The present invention is illustrated by way of the foregoing description and examples. The foregoing description is intended as a non-limiting illustration, since many variations will become apparent to those skilled in the art in view thereof. It is intended that all such variations within the scope and spirit of the appended claims be embraced thereby.

Changes can be made to the composition, operation and arrangement of the method of the present invention described herein without departing from the concept and scope of the invention as defined in the following claims.

Any references referred to herein are incorporated by reference.

WHAT IS CLAIMED IS:

1. A mutant protein derived from a wild-type human Bcl-2 protein wherein a sequence of amino acid residues comprising a flexible loop from said wild-type human Bcl-2 protein is replaced with a replacement amino acid sequence comprising at least two acidic amino acids.

2. The mutant protein of Claim 1 wherein said replacement amino acid sequence comprises a sequence of at least a portion of a flexible loop from human Bcl-x_L protein.

3. The mutant protein of Claim 2 wherein the replacement amino acid sequence comprises the sequence of SEQ ID NO:1.

4. The mutant protein of Claim 1 wherein the replacement amino acid sequence comprises a sequence of at least 4 to about 50 amino acid residues.

5. The mutant protein of Claim 1 wherein said replacement amino acid sequence comprises a sequence of at least 16 to about 25 amino acid residues.

6. The mutant protein of Claim 1 wherein said acidic amino acids are glutamic acid.

7. The mutant protein of Claim 1 wherein said acidic amino acids are aspartic acid.

8. The mutant protein of Claim 1 wherein said acidic amino acids are a glutamic acid and aspartic acid.

9. The mutant protein of Claim 1 wherein said amino acid residues which encode a flexible loop from said human Bcl-2 protein comprise amino acids 35-91 of said human Bcl-2 protein.

10. The mutant protein of Claim 1 which has an isoelectric point lower than that of wild-type Bcl-2.

11. The mutant protein of Claim 10 wherein said isoelectric point is from 4.5 to about 6.0.

12. The mutant protein of Claim 10 wherein said isoelectric point is from 5.0 to about 5.5.

13. The mutant protein of Claim 10 wherein said isoelectric point is 5.0.

14. A mutant protein having an amino acid sequence comprising:
MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDDVEENRTEAPEGTESEVVHLA
LRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGRFATVVEELFRDGVNWGRIVAFFEF
GGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVELYGPSMR
(SEQ ID NO:2).

15. An assay for identifying substances which bind to a Bcl-2 protein, the assay comprising the steps of:

(a) providing a candidate substance to be tested;

(b) providing a labeled peptide which is capable of binding tightly to said mutant protein of Claim 1;

(c) forming a complex of the labeled peptide with said mutant protein;

(d) forming a reaction mixture by contacting the candidate substance with the labeled peptide/mutant protein complex;

(e) incubating the reaction mixture under conditions sufficient to allow the candidate substance to react and displace the labeled peptide; and

(f) determining the amount of labeled peptide that has been displaced from binding to said mutant protein.

16. The assay of Claim 15 wherein the peptide is labeled with radioisotopes, fluorescent moieties, enzymes, specific binding molecules or particles.

17. The assay of Claim 16 wherein the peptide is labeled with a fluorescein compound.

18. The assay of Claim 17 wherein the peptide is labeled with fluorescein isothiocyanate or 5-carboxy-fluorescein.

Abstract

Mutant peptides derived from wild-type human Bcl-2 are disclosed. Assays to identify substances which block the ability of Bcl-2 to inhibit apoptosis also are disclosed.

FIGURE 1

	1				50
Bcl-2/iso1	MAHAGRTGYD	NREIVMKYIH	YKLSQRGYEW	DAGDVGAAPP	GAAPAPG**I**FS
Bcl-2/iso2	MAHAGRTGYD	NREIVMKYIH	YKLSQRGYEW	DAGDVGAAPP	GAAPAPG**I**FS
Bcl-2/iso3	MAHAGRTGYD	NREIVMKYIH	YKLSQRGYEW	DAGDVGAAPP	GAAPAPG**F**FS
Bcl-xL	MSMAMSQS	NRELVVDFLS	YKLSQKGYSW	SQFSDVEENR	TEAPEETESE
	51				100
Bcl-2/iso1	SQPGHTPHPA	ASRDPVARTS	PLQTPAAPGA	AAGPALSPVP	PVVHL**A**LRQA
Bcl-2/iso2	SQPGHTPHPA	ASRDPVARTS	PLQTPAAPGA	AAGPALSPVP	PVVHL**T**LRQA
Bcl-2/iso3	SQPGHTPHPA	ASRDPVARTS	PLQTPAAPGA	AAGPALSPVP	PVVHL**T**LRQA
Bcl-xL	METPSAINGN	PSWHLADSPA	VNGATGHSSS	LDAREVIP-M	AAVKQALREA
	101				150
Bcl-2/iso1	GDDFSRRYR**G**	DFAEMSSQLH	LTPFTARGRF	ATVVEELFRD	GVNWGRIVAF
Bcl-2/iso2	GDDFSRRYR**R**	DFAEMSSQLH	LTPFTARGRF	ATVVEELFRD	GVNWGRIVAF
Bcl-2/iso3	GDDFSRRYR**R**	DFAEMSSQLH	LTPFTARGRF	ATVVEELFRD	GVNWGRIVAF
Bcl-xL	GDEFELRYRR	AFSDLTSQLH	ITPGTAYQSF	EQVVNELFRD	GVNWGRIVAF
	151				200
Bcl-2/iso1	FEFGGVMCVE	SVNREMSPLV	DNIALWMTEY	LNRHLHTWIQ	DNGGWDAFVE
Bcl-2/iso2	FEFGGVMCVE	SVNREMSPLV	DNIALWMTEY	LNRHLHTWIQ	DNGGWDAFVE
Bcl-2/iso3	FEFGGVMCVE	SVNREMSPLV	DNIALWMTEY	LNRHLHTWIQ	DNGGWDAFVE
Bcl-xL	FSFGGALCVE	SVDKEMQVLV	SRIAAWMATY	LNDHLEPWIQ	ENGGWDTFVE
	201			239	
Bcl-2/iso1	LYGPSMRPLF	DFSWLSLKTL	LSLALVGACI	TLGAYLGHK	
Bcl-2/iso2	LYGPSMRPLF	DFSWLSLKTL	LSLALVGACI	TLGAYLGHK	
Bcl-2/iso3	LYGPSMRPLF	DFSWLSLKTL	LSLALVGACI	TLGAYLGHK	
Bcl-xL	LYGNNAAAES	RKGQERFNRW	FLTGMTVAGV	VLLGSLFSRK	

FIGURE 2

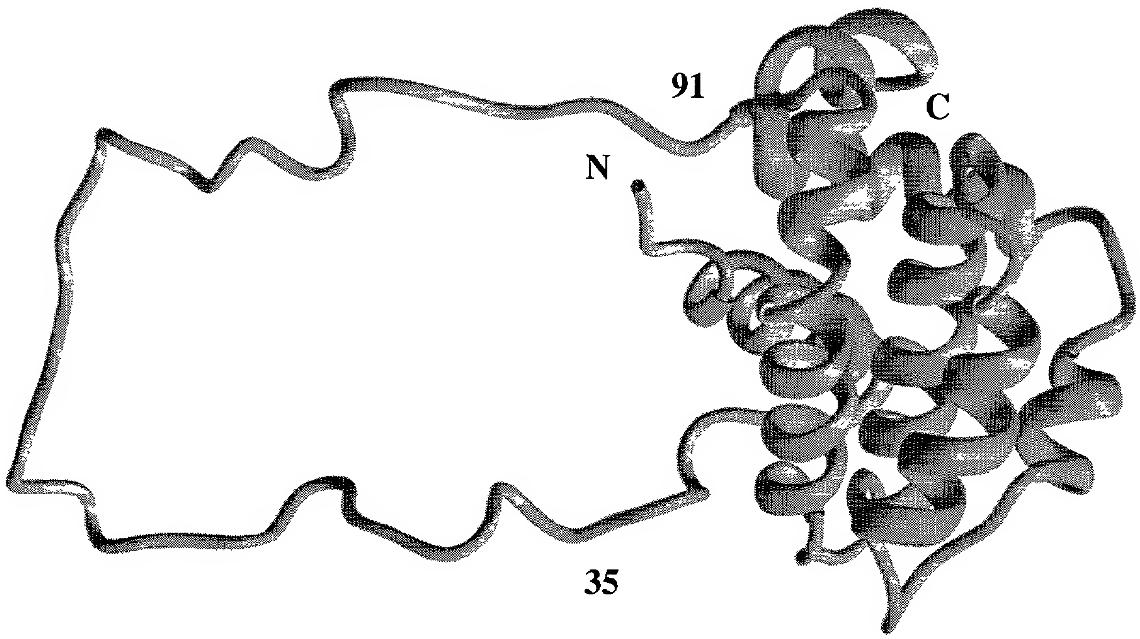
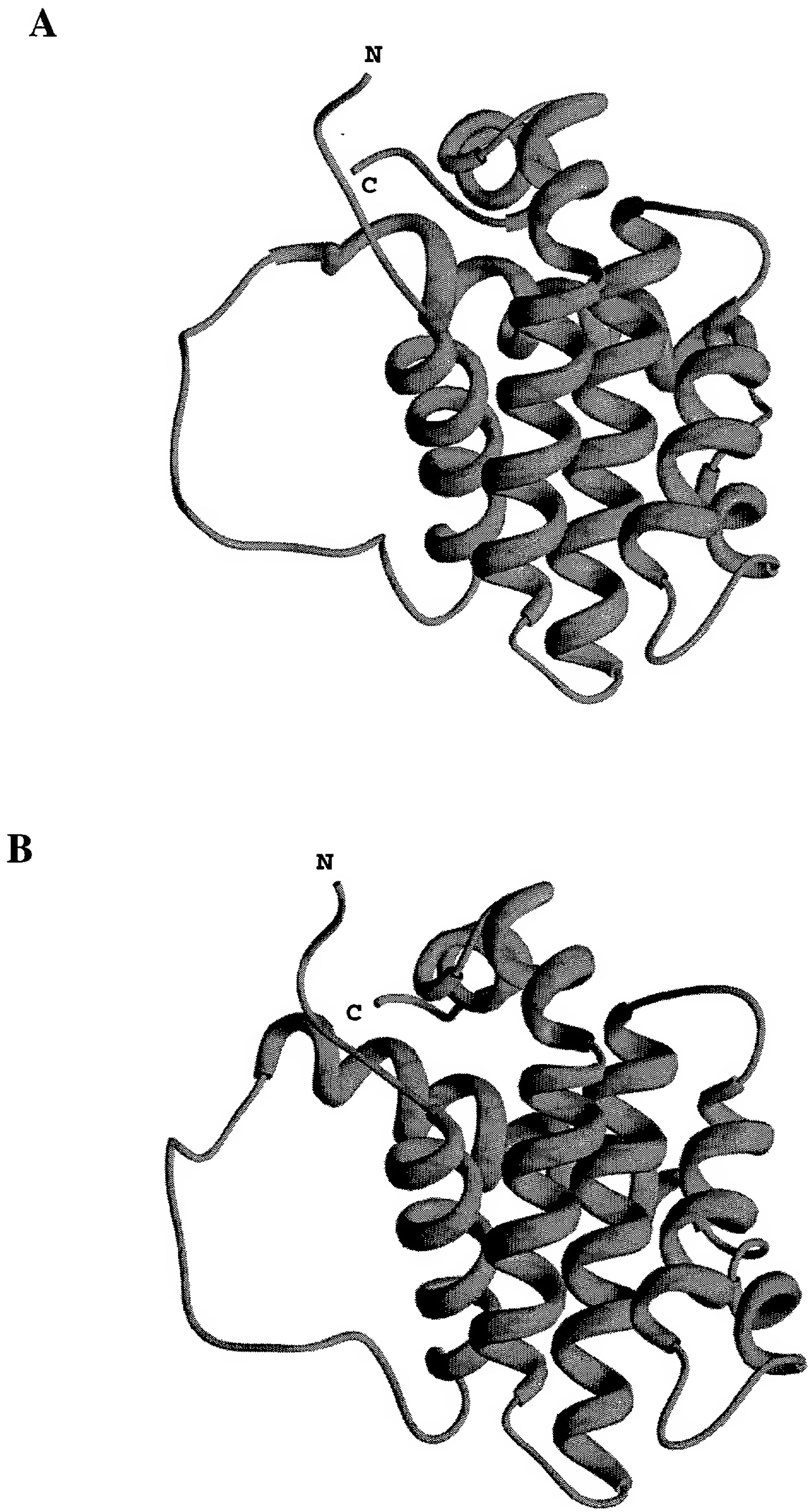


FIGURE 3



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Stephen W. Fesik, et al.

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Wanda E. Smith

Declaration and Power of Attorney for a United States Patent Application

As a below-named inventor, I hereby declare:

My residence, post office address and citizenship are as stated below next to my name. I believe I am an original and first and joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled, "MUTANT BCL-2 PROTEINS AND USES THEREOF", the specification of which is attached.

I hereby state that I have reviewed and understand the contents of the above-mentioned specification, including the claims.

I acknowledge a duty to disclose to the Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

Claim to benefit of foreign application(s) as follows:

I hereby claim foreign priority benefits under 35 U.S.C. §119 for the following foreign applications for patent or inventor's certificate.

NONE

The following foreign applications for patent or inventor's certificate have a filing date earlier than the filing date of the applications identified above.

NONE

Claim to benefit of earlier U.S. application(s) as follows:

I hereby claim benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

NONE

I hereby claim the benefit under 35 U.S.C. §120 of the following earlier-filed United States patent applications. Insofar as the subject matter of each of the claims of this application is not disclosed in the prior U.S. applications in the manner required by 35

U.S.C. §112, first paragraph, I acknowledge a duty to disclose to the Patent and Trademark Office all information known to me to be material to patentability as defined in 37 C.F.R. §1.56 which came into existence between the filing date(s) of the prior applications and the national or PCT filing date of this application.

NONE

I hereby appoint the following Attorneys and/or agents to prosecute this application and any continuation or divisional applications based hereon, and to transact all business in the Patent and Trademark Office connected therewith:

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I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that all statements made herein were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

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Stephen W. Fesik Date

11/20/00
Andrew M. Petros Date

11/20/00
Ho Sup Yoon Date

David G. Nettesheim 11/20/00
David G. Nettesheim Date

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<110> Fesik, Steven W.
Petros, Andrew M.
Yoon, Ho Sup
Nettescheim, David G.

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